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SEQUENCE LISTING

<110> US ONLY:
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5

OTHER COUNTRIES:
 Agriculture Victoria Services Pty Ltd AND Pig Research and Development
 Corporation AND Pfizer Products Inc.

10 <120> Novel therapeutic compositions for treating infection by *Lawsonia spp.*

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<150> AU PR1381

15 <151> 2000-11-10

<150> US 60/249596

<151> 2000-11-17

<160> 68

20 <170> PatentIn Ver. 2.0

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ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca	192
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 30 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
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	Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile	
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	115 120 125	
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	ata gaa agt gat ata gaa aaa cct gaa tca agt cct atc ttt agt aaa	336
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	aag ctt gaa acc tct gca gaa gaa gca cat ttt tat tat aat tcc att	720
	Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile	
	225 230 235 240	
50		
	aaa gaa gct gtt gca gct gct atc cga ggt tct aca cca atg ata gca	768
	Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala	
	245 250 255	
55		
	gta gaa tat gga aga cgt gcc ata cct aat aca ttt cgt cca tca ttt	816

45 Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile
165 170 175

- 16 -

Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu
180 185 190

5 Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr
195 200 205

Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser
210 215 220

10 Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile
225 230 235 240

Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala
15 245 250 255

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Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
40 20 25 30

gtt aaa gaa ggt ctt gct gca tat ttt tct tca tct gat gct aca ttt 144
Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
35 40 45

45 aaa aca cct gat agt tcg cca atc tct aac aat cct ctt atc aac caa 192

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- 17 -

Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
 50 55 60

5 ata gat aaa ctt gat act cga caa tta aaa att aat gaa aca gaa caa 240
 Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
 65 70 75 80

10 tct cat tat gct ctt gct aat aaa tta aaa aaa atg tta atg gct gat 288
 Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
 85 90 95

15 gct atc cca cag tca gca aca gga ata agt gct gac gat gtt ggt gta 336
 Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
 100 105 110

20 tta tta cgt gta aat tct aat tcc acg ttt ttt cct ggt aca gca act 384
 Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
 115 120 125

25 ctt aca ccc gaa ggg aaa aaa gtt atg gga act gtt tta gcc gtt ctc 432
 Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
 130 135 140

30 cgt gaa tat aat ctt tac ctt gtg ata cgt ggc cat gct gat att ggt 480
 Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
 145 150 155 160

35 gaa ata aca aaa ggc agc cct ttt gct tct aac tgg gaa ctt tca gga 528
 Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
 165 170 175

40 gct cgt gca gct gca gct gca cag tat ctt gta gag cac ggg ata aag 576
 Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
 180 185 190

45 gct tca cga att cgc tct gta gga tat gca gat aca aga cct cta gaa 624
 Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
 195 200 205

50 cct agt tct cct gaa gga agt aca aaa aat cgt cgt ata gaa ttc tat 672
 Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
 210 215 220

55 ttt cat cgg cca gaa gtt atg tct tat ggc gtt gta tat taa tag 717
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- 18 -

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 15 Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
 35 40 45

 Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
 50 55 60
 20 Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
 65 70 75 80

 Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
 25 85 90 95

 Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
 100 105 110

 30 Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
 115 120 125

 Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
 130 135 140
 35 Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
 145 150 155 160

 Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
 40 165 170 175

 Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
 180 185 190

 45 Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
 195 200 205

F00303E0-40004

- 19 -

Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
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tta tgc tca atg atg gaa gct gct ata tac tct atc cct att act tat 96
 Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
 25 20 25 30

att gaa cac ctt cgt gaa cag gga agc aaa aaa gga gaa aaa ctt tat 144
 Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
 35 40 45

30 tat tta cat agt aat att gat cag cct att aca gcc gta tta ata ttg 192
 Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
 50 55 60

35 aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct 240
 Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 65 70 75 80

aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc 288
 40 Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
 85 90 95

acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt 336
 Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
 45 100 105 110

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	Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser	
	115 120 125	
5	att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta	432
	Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu	
	130 135 140	
10	aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac	480
	Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp	
	145 150 155 160	
15	atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca	528
	Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro	
	165 170 175	
20	tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat	576
	Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr	
	180 185 190	
25	gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa	624
	Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu	
	195 200 205	
30	aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat	672
	Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr	
	210 215 220	
35	agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att	720
	Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile	
	225 230 235 240	
40	atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa	768
	Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu	
	245 250 255	
45	aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt	816
	Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser	
	260 265 270	
50	caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat	864
	Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His	
	275 280 285	
55	ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt gtt tcc	912
	Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser	

- 21 -

290 295 300

tta gaa gat gta tta gaa act atg ctt gga aga gaa att gtt gat gaa 960
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 5 305 310 315 320

agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt 1008
 Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
 325 330 335

10 gca tta atc caa aat aat aaa aat act ctt tta aaa taa 1047
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 340 345

15 <210> 14
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Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
 35 40 45

30 Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
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Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 35 65 70 75 80

Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
 85 90 95

40 Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
 100 105 110

Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
 115 120 125

45 Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu

10030160-110601

- 22 -

130 135 140

Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
 145 150 155 160

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 Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
 165 170 175

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 Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
 180 185 190

Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
 195 200 205

15
 Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
 210 215 220

20
 Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
 225 230 235 240

Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
 245 250 255

25
 Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
 260 265 270

Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
 275 280 285

30
 Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser
 290 295 300

35
 Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu
 305 310 315 320

Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
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 Ala Leu Ile Gln Asn Asn Lys Asn Thr Leu Leu Lys
 340 345

<210> 15
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<220>

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<222> (1)..(1809)

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<400> 15

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10

ata aca gaa aat tat ctc ttt gct aca tca att acc act tcc aca att 96
 Ile Thr Glu Asn Tyr Leu Phe Ala Thr Ser Ile Thr Thr Ser Thr Ile
 20 25 30

15

aac caa caa cat ata gca tat aca gtt act ttt acc tct cca gaa aat 144
 Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
 35 40 45

20

cct aat ctt gca aca gag atg gaa aca cat agt gaa tta gta aag ctt 192
 Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
 50 55 60

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gca aat caa tct tta gat agt aaa ata ggt tta aat tta cgt gtt aaa 240
 Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
 65 70 75 80

30

gaa gat ata agt aca gca caa aaa att ctt gac tcg aat ggt tat tat 288
 Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
 85 90 95

35

agt gga agt gtc gag gga aag att gac tgg cag acg aac cct att agt 336
 Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser
 100 105 110

40

atc caa atc caa ttt aaa cca aat gta caa tat aaa ata aat aca ata 384
 Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile
 115 120 125

45

cat atc caa tac ctt gat agt gaa ctt gca tat ctc cct ctt tcc tta 432
 His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu
 130 135 140

gaa gaa ttc aat ctc tct aaa ggt aat cct gct ctt gct gtt aat atc 480
 Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
 145 150 155 160

10010160-110904

- 24 -

cta tcc tct gta agt agc ctc atg caa tat ata cat aat aat gga tat 528
 Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr
 165 170 175

5 cca tta gcc aaa ata aaa aaa act caa tac ata att aat cgg atg gat 576
 Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
 180 185 190

10 tat aca ttt gat att gat tta gta ata aga caa gga ccg tta ctc cat 624
 Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
 195 200 205

15 atg ggt aaa gta caa cct caa cat aat ctc aat att tca aca ata ttc 672
 Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
 210 215 220

20 cta aat aaa att gct aca tgg aag gaa gga agg gta tgg aac aat gca 720
 Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala
 225 230 235 240

ctc ctt gat tct tat cga aca cgg ctt caa caa aca ggc ctt ttc agt 768
 Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser
 245 250 255

25 tct ata act ctc aat cca agg aat caa aaa gaa caa aat ggt aac acc 816
 Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr
 260 265 270

30 tct ata gaa ctt gtt gca aca gaa gcc cct cca agg act att agt ggt 864
 Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
 275 280 285

35 ggc tta caa tac tct tct gat caa ggt att ggt gca cgt ggg act tgg 912
 Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
 290 295 300

40 gaa cat cga aat gtt ttt ggt aat gga gaa ctt ttt cgt ata aca gca 960
 Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
 305 310 315 320

cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca 1008
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 325 330 335

45 gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa 1056
 Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys

10010160 - 110904

2025年12月31日

2025年12月31日

- 26 -

aaa ata aca gaa tcc att ggc att gtg cca att tat tgg atg ggg gaa 1632
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 530 535 540

5 tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg 1680
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 545 550 555 560

10 ggg gta ggc ctg ggg cta cga tat tat aca agt ttt gcc ccc ata cgt 1728
 Gly Val Gly Leu Gly Leu Arg Tyr Tyr Thr Ser Phe Ala Pro Ile Arg
 565 570 575

15 tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt 1776
 Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe
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20 caa ctt tat att agt att ggg caa gca ttc taa tga 1812
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35 Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
 35 40 45

Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
 50 55 60

40 Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
 65 70 75 80

Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
 85 90 95

45 Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser

10010160-110901

[illegible]

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	370				375				380							
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	Phe	Thr	Leu	Phe	Gly	Ile	Pro	Leu	Ser	Ile	Thr	Arg	Asp	Ser	Ser	Lys
					405				410				415			
	Asp	Pro	Leu	Asn	Pro	Ile	Gln	Gly	Thr	Lys	Ala	Thr	Leu	Asn	Val	Thr
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	435								440				445			
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	515								520				525			
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	530				535								540			
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	Gly	Val	Gly	Leu	Gly	Leu	Arg	Tyr	Tyr	Thr	Ser	Phe	Ala	Pro	Ile	Arg
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	Leu	Asp	Ile	Ala	Thr	Pro	Leu	Gln	Asp	Arg	Ser	His	Asn	Lys	His	Phe
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<213> Lawsonia intracellularis

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gca ttt acg tta ttt tta gga ctt att att aca ggc att ctt ttt ata 96

Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile

20 25 30

cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta 144

Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu

35 40 45

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ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca 192

Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro

50 55 60

30 ttc cca gaa caa att act att aat gaa ctt agc ctt agt gat gtg aat 240

Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn

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gga act tac ctt aca ata tct aac tta gaa atc caa tca aac tta tgg 288

35 Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp

85 90 95

gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat 336

Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp

100 105 110

ctt gta tta tat cgc tta ccc tca aat aat aat cta aaa aaa tca tct 384

Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser

115 120 125

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aca agt ttt gtg tta cct cac ata tca ttt gat tta act cca tgg tgg 432

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	Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu	
	145 150 155 160	
10	tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat	528
	Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp	
	165 170 175	
15	ggg aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac	576
	Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn	
	180 185 190	
20	aaa aca aaa att ata gga acg ctt cgt tac caa ggg aat aag aca caa	624
	Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln	
	195 200 205	
25	ttt ttt gaa tat gtt cat cct aca cgg ata gta aca cta gag ata gac	672
	Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp	
	210 215 220	
30	agc gta gct gat aaa aag tca tat aat aat agt atc ctt gaa caa cct	720
	Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro	
	225 230 235 240	
35	cta cat tta cac ctt tct att tat cct gaa cat aat aga att atc tta	768
	Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu	
	245 250 255	
40	cac tca tta cta gct gaa tat ggt agc tgg tta ctt aca tca gaa agt	816
	His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser	
	260 265 270	
45	att gaa gta tct aat gag caa tta aaa gga aat att tta tta aaa tat	864
	Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr	
	275 280 285	
50	aat gga gaa gct act cat caa ctt cct ata aaa aaa ctt aac tca tca	912
	Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser	
	290 295 300	
55	att acc ctc agt ggc tca cta aat aaa cct aat ttt agt ata caa atg	960
	Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met	
	305 310 315 320	

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- 31 -

5 aca tta cct gaa att aac att aca aaa aac ata ata gat ctt caa aca 1008
 Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr
 325 330 335

10 gaa ctt gtt att aat cta gga ctt ttc tct act cac tct gat att ctt 1056
 Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu
 340 345 350

15 aca tct ggg aca att aca gta cag gga gaa act ata ccc aat agt att 1104
 Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile
 355 360 365

20 ctt tcc agt gca gtt gat ata ata gcc tct aca aca aca cat aca att 1152
 Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr Thr His Thr Ile
 370 375 380

25 acc tta gag cat gca acc tta aca tct cca gaa atg cat ttt tcc cta 1200
 Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu
 385 390 395 400

30 tct gga gaa ttt aat agt ctt cta gga aat atc gat gca aac cta aaa 1248
 Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
 405 410 415

35 ggt aat act cca act ctt agt ata ttt tct tct ctt ctt gga cta cct 1296
 Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
 420 425 430

40 gat ctt act ggg caa agt aac att act ata gga tta cac cgt caa ggg 1344
 Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
 435 440 445

45 tct tcc tct tca ata gaa gga aca gca act gtc tca ctt aat aat atg 1392
 Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met
 450 455 460

50 aac tgg gga gta caa gca tta cag ggg aca tta ggt gat aat gca act 1440
 Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr
 465 470 475 480

55 cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta 1488
 Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu
 485 490 495

60 aac aaa ttg aaa tta aca gca aag aat gtt tat gct gaa ggc ctt att 1536

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Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
 500 505 510

5 aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct 1584
 Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro
 515 520 525

10 aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta 1632
 Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu
 530 535 540

15 att aca gtg tct gga aaa ctt gac gca cct tct ata gaa agc aaa att 1680
 Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile
 545 550 555 560

ttt tca tca caa ctc acc tgg aat gcg ctc caa ctt aat aat cct caa 1728
 Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln
 565 570 575

20 ctc ata ata act act act caa tct tct tcc tct gcg att aaa ggt aat 1776
 Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn
 580 585 590

25 ata aca ctc tcg gct gag cca gct tca tct gag gca tta acc ttt tca 1824
 Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
 595 600 605

30 agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata 1872
 Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
 610 615 620

35 gga aat ata tta gga gta aat ctt gat ggt aat att aaa ata aca aaa 1920
 Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys
 625 630 635 640

aaa gat tac ctt ata aat ggt gat att att gca gaa gtt cag tct tgg 1968
 Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp
 645 650 655

40 aaa gat att gca aac ata ttg caa ata cct att aga ggt tca gca tca 2016
 Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
 660 665 670

45 ata aaa ata cag ttt gat cca aag aat caa caa tgt att tct act caa 2064
 Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln
 675 680 685

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 100-30150-110994

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5 tgg caa tta aaa aat ttc ata tta ggt aat aat ttt aat gta act act 2112
 Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr
 690 695 700

10 ata aaa gga aga gca gat aca ata caa ctt cat aag aat cct aca att 2160
 Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile
 705 710 715 720

15 gct ctc tct tca aaa att ggt gct ggt aca tat gaa gac ttt caa tgg 2208
 Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp
 725 730 735

20 aca caa ggg acg tta gac ata aaa ggc aca tta aaa aat ttt aat agt 2256
 Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser
 740 745 750

25 aaa ata aat ata gca gga caa aca act gta aac gca aac ttt caa aca 2304
 Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr
 755 760 765

30 aat ctt ttt gaa aaa aat att aat ata act act ctt aat tta aaa aat 2352
 Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn
 770 775 780

35 att caa aaa aat ata gga att aag ctc ctt cag cca ata aaa att ata 2400
 Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile
 785 790 795 800

40 gtc tca cct caa caa ttt gtt ctt aat aac tgt tca cta gca att ctt 2448
 Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu
 805 810 815

45 cca tct gga aca att aca act gat ata tat gtt act cct caa cga ctt 2496
 Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu
 820 825 830

50 aat gct aat gca atc att aaa gaa gtt tca ctt ctc tct ttc caa cca 2544
 Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro
 835 840 845

55 ttt agt ata ctt ctt cct caa gga aat ata aat gga cac ata aca ctt 2592
 Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu
 850 855 860

60 aca gga ata cct agt aaa cct aaa gga aca ctc tca ttt gat att cta 2640

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Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu
865 870 875 880

5

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4.

ctt att ggt aat att ggc tca tct aaa gaa cac ttt cct ttg tct att 3168
45 Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile
 1045 1050 1055

- 35 -

45

- 36 -

Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
1235 1240 1245

5 ata gtt tcc caa gtt ctt ttt ggt aaa agc tca caa agt ctt agc agg 3792
Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg
1250 1255 1260

10 ata caa gcc ata caa ctt gct caa gaa tta gca aac tta aca gga ttt 3840
Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe
1265 1270 1275 1280

15 aat act gga agt atg aat ttc cta aca aat att cga cag aca tta ggg 3888
Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly
1285 1290 1295

20 tta gat ata ctt agc tta ggg aca act tct aat aga aaa gcc aat aca 3936
Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr
1300 1305 1310

25 tcc aac tca aac gat caa ata gaa gat atc cct gtt ata gaa cta ggt 3984
Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Leu Gly
1315 1320 1325

30 aaa tat att aca gac act gtt tat gtt ggt gtt gaa caa agt tat tta 4032
Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
1330 1335 1340

35 gat agt aat gat act ggg gca aga ata tca gtt gaa ctt gca cct aat 4080
Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
1345 1350 1355 1360

40 ttt aat ctt gaa ggt aga aca ggg act caa tat agt gag ata ggt att 4128
Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile
1365 1370 1375

45 aat tgg aaa aaa gat tat taa 4149
Asn Trp Lys Lys Asp Tyr
1380

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10010160-110901

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5	Ala	Phe	Thr	Leu	Phe	Leu	Gly	Leu	Ile	Ile	Thr	Gly	Ile	Leu	Phe	Ile
				20					25					30		
	Arg	Thr	Ser	Thr	Gly	Ile	Ala	Trp	Ile	Lys	Asn	Thr	Val	Ser	Ser	Leu
			35					40					45			
10	Leu	Gln	Gln	Gln	Gly	Ile	Ile	Leu	Gln	Val	Ser	Ser	Ile	Ile	Gly	Pro
		50					55					60				
	Phe	Pro	Glu	Gln	Ile	Thr	Ile	Asn	Glu	Leu	Ser	Leu	Ser	Asp	Val	Asn
	65					70					75					80
15	Gly	Thr	Tyr	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Ile	Gln	Ser	Asn	Leu	Trp
					85					90					95	
	Ala	Leu	Phe	Lys	Gly	Gln	Leu	Glu	Ile	Leu	Ser	Phe	Glu	Leu	Asn	Asp
20				100				105						110		
	Leu	Val	Leu	Tyr	Arg	Leu	Pro	Ser	Asn	Asn	Asn	Leu	Lys	Lys	Ser	Ser
			115					120					125			
25	Thr	Ser	Phe	Val	Leu	Pro	His	Ile	Ser	Phe	Asp	Leu	Thr	Pro	Trp	Trp
		130					135					140				
	Thr	Glu	His	Ile	Arg	Ile	Gln	Asn	Ile	His	Ile	Asn	Asn	Thr	Gln	Leu
	145					150				155						160
30																
	Ser	Ser	Asp	Ile	Ile	Gly	Ile	Pro	Leu	Val	Leu	Ser	Leu	Glu	Gly	Asp
					165					170					175	
	Gly	Thr	Leu	Thr	Asn	Trp	Asn	Gly	Thr	Phe	Gln	Leu	Ser	Ser	Ser	Asn
35				180					185					190		
	Lys	Thr	Lys	Ile	Ile	Gly	Thr	Leu	Arg	Tyr	Gln	Gly	Asn	Lys	Thr	Gln
		195						200					205			
40	Phe	Phe	Glu	Tyr	Val	His	Pro	Thr	Arg	Ile	Val	Thr	Leu	Glu	Ile	Asp
		210					215					220				
	Ser	Val	Ala	Asp	Lys	Lys	Ser	Tyr	Asn	Asn	Ser	Ile	Leu	Glu	Gln	Pro
	225					230					235					240
45																
	Leu	His	Leu	His	Leu	Ser	Ile	Tyr	Pro	Glu	His	Asn	Arg	Ile	Ile	Leu

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245 250 255
 His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser
 260 265 270
 5
 Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr
 275 280 285
 Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser
 10 290 295 300
 Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met
 305 310 315 320
 15 Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr
 325 330 335
 Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu
 340 345 350
 20 Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile
 355 360 365
 Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr Thr His Thr Ile
 25 370 375 380
 Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu
 385 390 395 400
 30 Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
 405 410 415
 Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
 420 425 430
 35 Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
 435 440 445
 Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met
 40 450 455 460
 Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr
 465 470 475 480
 45 Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu
 485 490 495

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Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
 500 505 510

5 Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro
 515 520 525

Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu
 530 535 540

10 Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile
 545 550 555 560

Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln
 15 565 570 575

Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn
 580 585 590

20 Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
 595 600 605

Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
 610 615 620

25 Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys
 625 630 635 640

Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp
 30 645 650 655

Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
 660 665 670

35 Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln
 675 680 685

Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr
 690 695 700

40 Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile
 705 710 715 720

Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp
 45 725 730 735

10030130-110901

Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser
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5

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Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser
965 970 975

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	980	985	990
	Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu		
	995	1000	1005
5	Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile		
	1010	1015	1020
	Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln		
10	1025	1030	1035 1040
	Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile		
	1045	1050	1055
15	Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser		
	1060	1065	1070
	Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser		
20	1075	1080	1085
	Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr		
	1090	1095	1100
	Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr		
25	1105	1110	1115 1120
	Gln Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr		
	1125	1130	1135
30	Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser		
	1140	1145	1150
	Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile		
35	1155	1160	1165
	Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe		
	1170	1175	1180
	Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe		
40	1185	1190	1195 1200
	Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr		
	1205	1210	1215
45	Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser		
	1220	1225	1230

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Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
1235 1240 1245

5 Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg
1250 1255 1260

Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe
1265 1270 1275 1280

10 Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly
1285 1290 1295

Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr
15 1300 1305 1310

Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Leu Gly
1315 1320 1325

20 Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
1330 1335 1340

Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
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30 1380

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Oligonucleotide probe/primer

40 <400> 19
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:

5 Oligonucleotide probe/primer

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21

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<210> 21

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15

<220>

<223> Description of Artificial Sequence:

Oligonucleotide probe/primer

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<400> 21

gctcatctaa agaacacttt cc

22

<210> 22

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<211> 23

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<223> Description of Artificial Sequence:

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caaggtagta tacaacttat tgg

23

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<210> 23

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:

Oligonucleotide probe/primer

45

<400> 23

F0033360-110901

23

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22

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45

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Oligonucleotide probe/primer

<400> 27

aagaatgcct gtaataataa gtcc

24

10 <210> 28

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20 ttgggggaatc ctacctacg

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<223> Description of Artificial Sequence:

30	Oligonucleotide probe/primer
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tattaggagt aaatcttgat g

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35

<210> 30

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:

Oligonucleotide probe/primer

45 <400> 30

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22

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	<211> 20	<212>
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45	<213> Artificial Sequence	

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<220>

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15 <223> Description of Artificial Sequence:
Oligonucleotide probe/primer

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20

<210> 36

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Oligonucleotide probe/primer

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35 <210> 37

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Oligonucleotide probe/primer

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45 attaggtgca agttcaactg

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- 48 -

<210> 38
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 15 <210> 39
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<223> Description of Artificial Sequence:
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<223> Description of Artificial Sequence:
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40 <223> Description of Artificial Sequence:
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<212> DNA

<213> Artificial Sequence

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 $\langle 220 \rangle$

<223> Description of Artificial Sequence:

Oligonucleotide probe/primer

10

<400> 45

ccttggttaa taacaatatc g

21

<210> 46

15

<211> 23

<212> DNA

<213> Artificial Sequence

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20

<223> Description of Artificial Sequence:

Oligonucleotide probe/primer

<400> 46

caactccact tcaagataga agc

23

25

<210> 47

<211> 29

<212> DNA

<213> Artificial Sequence

30

<220>

<223> Description of Artificial Sequence: oligo

<400> 47

35

gaccatggaa aaagtatggt attttttttc

29

<210> 48

<211> 36

<212> DNA

40

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligo

45

<400> 48

gaggatcctc tagagttaga atgcttgccc aatact

36

[illegible]

- 51 -

<210> 49
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 5 <213> Artificial Sequence

 <220>
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 10 <400> 49
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 <210> 50
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 15 <212> DNA
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 <220>
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 20
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 ttgaccatgg ctacatcaat taccacttcc ac 32

 <210> 51
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 ggacatatga ataacacaaa aataactttc 29

 35 <210> 52
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 40 <220>
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 45
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10010360-100001
 10010360-100001

- 52 -

<211> 32

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Description of Artificial Sequence: oligo

<400> 53

ggacatatgc ggacctctac aggcattgct tg

32

10

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence: oligo

<400> 54

tgaggattat taagttggag

20

20

<210> 55

<211> 20

25 <212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: oligo

<400> 55

gcatgcaacc ttaacatctc

20

30

<210> 56

35 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

40 <223> Description of Artificial Sequence: oligo

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45 <210> 57

<211> 20

F0040360-10504

- 53 -

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Description of Artificial Sequence: oligo

<400> 57

tctgcccata tcaagtggac

20

10 <210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

15 <220>

<223> Description of Artificial Sequence: oligo

<400> 58

ggaacatttc aactatcctc

20

20

<210> 59

<211> 28

<212> DNA

<213> Artificial Sequence

25

<220>

<223> Description of Artificial Sequence: oligo

<400> 59

gtaaggtgaag ttccattcac

20

30

<210> 60

<211> 25

<212> DNA

<213> Artificial Sequence

35

<220>

<223> Description of Artificial Sequence: oligo

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40 caacgtggat ccgaattcaa gcttc

25

<210> 61

<211> 17

45 <212> PRT

<213> Artificial Sequence

100-30-150-110904

- 54 -

<220>

<223> Description of Artificial Sequence: Peptide

5 <400> 61

Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Leu Thr

1 5 10 15

Met

10

<210> 62

<211> 7

15 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

20

<400> 62

Ala Thr Ser Ile Thr Thr Ser

1 5

25

<210> 63

<211> 45

<212> PRT

<213> Artificial Sequence

30

<220>

<223> Description of Artificial Sequence: Peptide

<400> 63

35 Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser

1 5 10 15

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp

20 25 30

40

Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met

35 40 45

45 <210> 64

<211> 50

40010160-410001

<212> PRT

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<400> 64

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15

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<210> 65

<211> 7

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Peptide

<400> 65

30 Glu Phe Asn Leu Ser Lys Gly
 1 5

<210> 66

35 <211> 17

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

40 <223> Description of Artificial Sequence: Peptide

<400> 66

Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Gly His
1 5 10 15

45

Met

- 56 -

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5  <210> 67
    <211> 7
    <212> PRT
    <213> Artificial Sequence

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10 <223> Description of Artificial Sequence: Peptide

<400> 67
 Arg Thr Ser Thr Gly Ile Ala
 1 5
 15

20

<210>	68
<211>	21
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

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25      <400> 68
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          1                      5                      10                      15

      His His His His His
30          20

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